

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:20:13 ; Search time 52.2 Seconds  
(without alignments)  
27.316 Million cell updates/sec

Title: US-09-331-631a-38

Perfect score: 53

Sequence: 1 CXXXCXXXXXXXXXXXXCXXC 21

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_66: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	30	2 A38933	vitronectin - bovi
2	53	100.0	37	2 E44007	aptoctoxin III - tr
3	53	100.0	39	1 IZMS	cygnin - black swa
4	53	100.0	40	2 JX0070	melagrin - turkey
5	53	100.0	55	2 S25774	testis-specific pr
6	53	100.0	57	1 SMK25	metallochionein 2
7	53	100.0	57	2 S59073	metallochionein 1s
8	53	100.0	58	1 SMKDIS	metallochionein 1
9	53	100.0	58	2 S59072	metallochionein 1s
10	53	100.0	58	2 A37039	metallochionein 1
11	53	100.0	58	2 S43367	metallochionein -
12	53	100.0	63	2 S25772	testis-specific pr
13	53	100.0	63	2 A34484	metallochionein 1
14	53	100.0	66	2 T18117	hypothetical prote
15	53	100.0	68	2 S25775	testis-specific pr
16	53	100.0	70	1 XISR1A	insect toxin 1 - s
17	53	100.0	70	1 S08267	toxin 1 - scorpion
18	53	100.0	72	2 S39416	metallochionein 10
19	53	100.0	72	2 S39418	metallochionein 10
20	53	100.0	72	2 S39419	metallochionein 10
21	53	100.0	72	2 S39417	metallochionein 10
22	53	100.0	74	2 S25773	testis-specific pr
23	53	100.0	83	2 A49763	midgut expression
24	53	100.0	84	2 J01356	VI protein - Misca
25	53	100.0	88	2 G34444	insect toxin 2 pre
26	53	100.0	95	1 KRDKF4	keratin B-4, feath
27	53	100.0	95	1 KRPFY4	keratin B-4, feath
28	53	100.0	98	1 KRCHP1	keratin I, feather
29	53	100.0	98	1 KRCHP2	keratin II, feather

30	53	100.0	98	1 KRGLBS	keratin, feather -
31	53	100.0	98	2 S06807	keratin, feather (
32	53	100.0	98	2 S06806	keratin, feather (
33	53	100.0	98	2 S06808	keratin, feather (
34	53	100.0	105	2 S64495	hypothetical prote
35	53	100.0	107	2 S17698	tap1 protein - gar
36	53	100.0	107	2 T27988	hypothetical prote
37	53	100.0	117	2 S24023	dopamine receptor
38	53	100.0	117	2 S24194	dopamine receptor
39	53	100.0	117	2 S24195	dopamine receptor
40	53	100.0	118	2 S26689	hypothetical prote
41	53	100.0	135	2 T15610	hypothetical prote
42	53	100.0	137	2 T15609	hypothetical prote
43	53	100.0	151	2 S60314	hair keratin cyste
44	53	100.0	152	2 T18975	hypothetical prote
45	53	100.0	153	2 PN0564	von Willebrand fac

#### ALIGNMENTS

RESULT 1  
A38933  
vitronectin - bovine (fragment)  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 05-Apr-1995 #sequence\_revision 05-Apr-1995 #text\_change 07-May-1999  
C/Accession: A38933; A32200; S22231; S15978  
R/Hayman, E.G.; Pierschbacher, M.D.; Suzuki, S.; Ruoslahti, E.  
Exp. Cell Res. 160, 245-258, 1985  
A/Title: Vitronectin-a major cell attachment-promoting protein in fetal bovine serum  
A/Reference number: A38933; MUID:86005161  
A/Accession: A38933  
A/Molecule type: protein  
A/Residues: 1-30 <HAY>  
R/Mimuro, J.; Loskutoff, D.J.  
J. Biol. Chem. 264, 936-939, 1989  
A/Title: Purification of a protein from bovine plasma that binds to type 1 plasminoge  
ctin.  
A/Reference number: A32200; MUID:89093166  
A/Accession: A32200  
A/Molecule type: protein  
A/Residues: 1-4, 'X', 6-8, 'X', 10-18, 'X', 20, 'X', 22-24, 'X', 26-28 <MIM>  
R/Nakashima, N.; Miyazaki, K.; Ishikawa, M.; Yatonjo, T.; Ogawa, H.; Uchibori, H.; Ma  
Blochin. Biophys. Acta 1120, 1-10, 1992  
A/Title: Vitronectin diversity in evolution but uniformity in ligand binding and size  
A/Reference number: S21768; MUID:92207982  
A/Accession: S22231  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 'X', 2-4, 'X', 6-8, 'X', 10-18, 'X', 20, 'X' <NAK>  
R/Seifert, D.; Loskutoff, D.J.  
Biochim. Biophys. Acta 1078, 23-30, 1991  
A/Title: Kinetic analysis of the interaction between type 1 plasminogen activator inh  
of bovine vitronectin.  
A/Reference number: S15978; MUID:91265534  
A/Accession: S15978  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-4, 'X' <SEI>  
C/Superfamily: vitronectin; hemopexin repeat homology; somatomedin B homology  
C/Keywords: cell adhesion; heparin binding

Query Match 100.0%; Score 53; DB 2; Length 30;  
Best local similarity 23.8%; Pred. No. 1.3e+02;  
Matches 5; Conservative 16; Mismatches 0; Indels 0; Caps 0;

OY 1 CXXXCXXXXXXXXXXXXCXXC 21  
DB 5 CKGRCTGFYATRCQCDELIC 25  
RESULT 2

E44007  
aplotoxin III - trap-door spider (Aptostichus sp.)  
N:Alternate names: insecticidal peptide Aps III  
C:Species: Aptostichus sp.  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999  
C:Accession: E44007  
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Quistad, G.B.  
Toxicom 30, 1043-1050, 1992  
A:Title: Identification of insecticidal peptides from venom of the trap-door spider, Aptostichus  
A:Reference number: A44007; MUID:93069259  
A:Accession: E44007  
A:Molecule type: protein  
A:Residues: 1-37 <SKI>  
A:Cross-references: PIDN:AAB24051.I; PID:9259281  
A:Note: the source is designated as Aptostichus schlinger1  
A:Note: sequence extracted from NCBI backbone (NCBIF:119526)  
C:Keywords: disulfide bond; toxin; venom

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Query Match          100.0%  Score 53:  DB 2:  Length 37:
Best Local Similarity 19.0%  Pred. No. 1.4e+02:
Matches      4:  Conservative      17:  Mismatches      0:  Indels      0:
                                Gaps      0:

Oy      1  CXXXXXXXXXXXXXXXXCXXC 21
         |::|::|::|::|::|::|::|
Db      15  CGGKCAINWMNCITGGGCCSKTC 35

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RESULT      3
1ZMS
cygnin - black swan
C:Species: Cygnus atratus (black swan)
C:Date: 18-Apr-1984 #sequence_revision 28-Feb-1986 #text_change 24-Nov-1999
C:Accession: A03258
R:Simpson, R.J.: Morgan, F.J.
submitted to the Atlas, November 1982
A:Reference number: A94600
A:Accession: A03258
A:Molecule type: protein
A:Residues: 1-39 <SIM>
C:Comment: Cygnin shows some similarity to the amino-terminal fragment of the carboxyl-1-
C:Superfamily: cygnin
C:Keywords: blocked amino end; egg white
E:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu

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Query Match          100.0%; Score 53; DR 1; Length 39;
Best Local Similarity 19.0%; Pred. NO. 1.4e+02;
Matches      4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

          1 CXXXCXXXXXXXXXXCXXC 21
            |:::|:::|:::|:::|
Db         12 CSSKCSKADVWSLSSDCKFC 32

RESULT      4
JX0070
meleagrin - turkey
N:Alternate names: cygnin homolog
C:Species: Meleagris gallopavo (common turkey)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Aug-1994
C:Accession: JX0070
R:Odani, S.; Koide, T.; Ono, T.; Takahashi, Y.; Suzuki, J.
J. Biochem. 105, 660-663, 1989
A:Title: Covalent structure of a low-molecular-mass protein, meleagrin, present in a tur
A:Reference number: JX0070; MUID:89340398
A:Accession: JX0070
A:Molecule type: protein
A:Residues: 1-40 <ODA>
C:Superfamily: cygnin
C:Keywords: egg white; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6-32,16-33/Disulfide bonds: (or 6-33, 16-32) #status predicted

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F;12-28/Disulfide bonds: #status experimental

Query Match	100.0%	Score 53;	DB 2;	length 40;
Best Local Similarity	19.0%;	Pred. NO. 1.5e+02;		
Matches	4;	Conservative	17;	Mismatches 0;
			Indels	0;
			Gaps	0;

```
QY 1 CXXXXXXXXXXXXXXXXCXXC 21
    |::|:::|:::|:::|:::|
Db 12 CSSKCSKAEWAYSPDCKVHC 32
```

RESULT 5  
S25774  
testis-specific protein Mst84Dc - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 20-Aug-1999  
C:Accession: S25774; C56565  
R:Kuhn, R.; Kuhn, C.; Boersch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M.  
Mech. Dev. 35, 143-151, 1991  
A:Title: A cluster of four genes selectively expressed in the male germ line of *Drosophila*  
A:Reference number: A56365; MUID:92102953  
A:Accession: S25774  
A:Molecule type: DNA  
A:Residues: 1-55 <KUH>  
A:Cross-references: EMBL:X67703; NID:911072; PIDN:CAA7939.1; PID:q11075  
A>Note: the authors translated the codon TGC for residue 55 as Thr  
A>Note: Sequence extracted from NCBI backbone (NCBIN:74217, NCBIPI:74222)  
C:Genetics:  
A:Gene: Mst84Dc  
A:Cross-references: Flybase:FBgn0004174  
A:Map position: 3  
C:Superfamily: fruit fly testis-specific protein  
C:Keywords: spermatogenesis; tandem repeat

Query Match	100.0%;	Score 53;	DB 2;	Length 55;
Best Local Similarity	19.0%;	Pred. No. 1.7e+02;		
Matches	4;	Conservative 17;	Mismatches 0;	Indels 0;
			Gaps 0;	

```
QY 1 CXXCXXXXXXCXXC 21
    |::|:::|:::|:::|
Db 2 CCGPCGSCGYCCGPCG 22
```

RESULT 6  
SMKD2S  
metallothionein 2 - mud crab  
C:Species: Scylla serrata (mud crab)  
C:Date: 19-Feb-1984 #sequence\_revision 19-Feb-1984 #texl\_change 13-Sep-1996  
C:Accession: A03284  
R:lerch, K.; Ammer, D.; Olafson, R.W.  
J. Biol. Chem. 257, 2420-2426, 1982  
A:Title: Crab metallothionein. Primary structures of metallothioneins 1 and 2  
A:Reference number: A92363; MUID:82142340  
A:Accession: A03284  
A:Molecule type: protein  
A:Residues: 1-57 <LER>  
C:Superfamily: metallothionein  
C:Keywords: metal binding

Query Match	100.0%;	Score 53;	DB 1;	length 57;
Best Local Similarity	19.0%;	Pred. No. 1.8e+02;		
Matches	4;	Conservative 17;	Mismatches 0;	Indels 0;
			Gaps 0;	

```
Qy 1 CXXXXXXXXXXXXXXXXCXXC 21
    |::|:::|:::|:::|:::|
Db 33 CSSGCKCANKEDCRKTCSPC 53
```

RESULT  
S59073



